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## THAT WHICH IS CLAIMED IS:

- 1. A method of regulating protein synthesis in situ comprising:
- (a) determining the sequence of musical notes associated with the amino acid chain of a protein by associating with each amino acid a musical note whose frequency is transposed from the proper frequency of the amino acid:
- (b) determining the musical periods of said sequence of musical notes by identifying similar series of musical notes;
  - (c) comparing the repartition of said musical sequence of said amino acid chain to the average repartition of said musical notes of the whole of proteins so as to determine the tone quality; and
  - (d) regulating the biosynthesis of said protein by playing said sequence of musical notes, including the musical period of said notes and the tone quality of said musical notes.
- 2. The method of regulating protein synthesis according to Claim 1 further comprising:

determining the lengths of said musical notes by rectifying collectively, and then rectifying individually said musical periods by adjusting the phrasing to the measure of said musical sequence.

3. The method of regulating protein synthesis according to Claim 1 further comprising determining the frequency of said musical note according to a code comprising:

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- (a) taking the frequency of each amino acid in its free state, proportional to its mass,
- (b) minimizing the global harmonic distance between the frequencies of each pair of amino acids in said protein while taking into account the proportion of each amino acid in the population of transfer RNAs within a cell where synthesis of said protein takes place, and wherein the displacement of the note frequency towards its synchronized value is inferior to half the interval between the two synchronized frequencies which surround said keynote frequency, then
- (c) transposing the frequencies thus obtained into the auditive range, said code being relative to the biosynthetic stimulation of said protein; and
- (d) obtaining said code relative to its inhibition by symmetrization of the logarithms of heretofore obtained frequencies with respect to their central value considered as the origin.
- 4. The method of Claim 3, wherein said code

  20 comprises the following notes of the chromatic tempered scale in ascending order:

Gly = low A; Ala = C; Ser = E; Pro, Val, Thr, Cys = F; Leu, Ile, Asn, Asp = G; Gln, Lys, Glu, Met = A; His = B flat; Phe as well as SeC = B; Arg, tyr = sharp C; Trp = sharp D.

5. The method of Claim 3, wherein said code comprises the following notes of a chromatic tempered scale, in ascending order:

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Trp = C; Arg, Tyr = D; Phe as well as SeC =
E flat; His = E; Gln, Lys, Glu, Met = F;
Leu, le, Asn, Asp = G; Pro, Val, Thr, Cys =
A; Ser = B flat; Ala = Sharp D; Gly = sharp
F,

which are deduced from the notes of the code by taking the notes of the chromatic tempered scale which are symmetrical to those of said keynotes with respect to central G.

- 6. The method according to Claim 3 wherein said synthesis stimulates synthesis of a protein in a plant.
  - 7. The method according to Claim 1, wherein each sound transposition of quantum vibrations associated with the biosynthesis of a given protein is completed by the color transposition of quantum vibrations associated to the mature protein after it is spatially folded back over itself, according to a code specific to the stabilization of that protein or to the inhibition of its biosynthesis obtained through the musical sequence realized according to Claim 1, which code is deduced from the code obtained from Claim 1, by application of the formula  $\nu \cong \nu_0$  Argch  $(e^{f/f}_0)^{\text{Logch 1}}$ , where f,  $f_0$  are the musical frequencies and  $\nu$ ,  $\nu_0$  the frequencies of colors, with the index  $_0$  showing the central values.
- 8. The method according to Claim 6, wherein the stabilization of proteins stimulated by the musical sequences obtained according to Claim 1 consists in the association to the different amino acids of the following colors:

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Gly = dark red; Ala = bright red; Ser = orange;
Pro, Val, Thr, Cys = ochre; Leu, Ile, Asn, Asp =
lemon yellow; Gln, Glu, Lys, Met = green; His =
emerald; Phe = blue; Arg, Tyr = indigo; Trp = purple

- 9. Transcriptions of a musical sequence according to Claim 1 selected from the group consisting of musical scores of said musical sequence and audio recordings of music according to said musical sequence.
- characterization of proteic sequences fit to be regulated by using any of the transcriptions characterized in that one delimits their metabolic role by decoding with the method according to Claim 3, thereby showing the musical similarities and anti-similarities that they present with other proteins, the harmonic superpositions with other proteic melodies, or a combination of these factors, from which the agonisms and antagonisms can be deduced.
  - 11. The method according to Claim 9, in which the characterization for a given application is refined by bipolar differential comparisons with the positive or negative effects obtained by using said transcriptions.
  - 12. The method according to Claim 10, in which the characterization for a given application is refined by identification, through musical similarity or antisimilarity of the proteins involved during positive or negative effects due or associated to acoustic or electromagnetic phenomena exhibiting distinct series of frequencies.